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SEP 9

PATENT

Appl. No. 09/438,185

TECH CENTER 1600/2900

Replacement Pages to the Specification:

Please replace pages 37 and 123 with the following replacement pages, together with annotated sheets showing changes in highlights. The replacement pages and annotated pages are attached to this amendment.

Attachment: Replacement Sheets

Annotated Sheets Showing Changes



SEP 9 2003

TECH CENTER 1600/2900

tRNAs

,5				0.1
tRNA#	<u>Begin</u>	<u>End</u>	<u>Type</u>	Codon
1	89657	89728	Thr	GGT
2	90998	91070	Trp	CCA
3	199301	199229	Met	CAT
4	199390	199317	Met	CAT
5	296075	296147	Val	TAC
6	296151	296224	Asp	GTC
7	409848	409922	Pro	TGG
8	462141	462214 Arg		CCT
9	672236	672318	Leu	CAA
10	677264	677337	Arg	TCG
11	739403	739486	Leu	CAG
12	781610	781680	Gly	TCC
13	784822	784896	Glu	TTC
14	784922	. 784994	Lys	TTT
15	836119	836191	Ala	GGC
16	843926	843999	Pro	GGG
17	877400	877473	Arg	ACG.
18	1085605	1085676	Gln	TTG
19	1142034	1142118	Ser	TGA
20	1175863	1175944	Leu	TAG
21	1230028	1229942	Ser	CGA
22	1137462	1137389	Val	GAC
23	1030603	1030533	Cys	GCA
24	1000022	999949	His	GTG
25	961607	961536	Gly	GCC
26	807413	807341	Arg	TCT
27	786780	786708	Thr	CGT
28	715971	715889	Leu	TAA
29	708441	708354	Ser	GCT
30	680259	680178	Leu	GAG
	631445	631373	Phe	GAA
32	626987	626901	Ser	GGA
33	293477	293405	Thr	TGT
34	293399	293317	Tyr	GTA
35	269142	269070	Ala	TGC
36	269065	268992	Ile	GAT
37	1643089	164318	Asn	GTT
38	87522	87450	Met	CAT





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TABLE 2

TECH CENTER 1600/2900

4DEN Gene #	From	To	Strand	Gene Function (C. Trachomatis Ortholog in parenthesis)
CPn0001	282	4	R	CT001 hypothetical protein
	573	875	F	gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002)
CPn0002	373 895	2370	F	gatA-Glu tRNA Gln Amidotransferae-(CT003)
CPn0003			F	gatB-(Pet 112) Glu tRNA Gln Amidotransferase (B Subunit)
CPn0004	2370	3833	F	pmp_1-Polymorphic Outer Membrane Protein G Family
CPn005	4127	6892	r R	pmp_1-1 drymorphic outer informer rotem or anning
CPn006	7293	7141		
. CPn007	7605	10496	F	
CPn008	10975	11685	F	
CPn009	11815	13119	F	•
CPn0010	13435	14325	F	c 1:0 :4 0010
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP [leader (14) peptide: outer membrane] - (CT351)
CPn0021	34410	32707	R	Predicted OMP [leader (19) peptide] - (CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R	yjjK/alr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	R	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	lon-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0038	52119	53831	F	ptsI-PTS PEP Phosphotransferase-(CT336)
CPn0039	54250	53963	R	ybaB-(CT335)

REPLACEMENT PAGE 37 (1 of 2)





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TECH CENTER 1600/2900

TABLE 2

Gene #	From	То	Strand	Gene Function (C. Trachomatis Ortholog in parenthesis)
CPn0001	282	4	R	CT001 hypothetical protein
CPn0002	573	875	F	gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002)
CPn0003	895	23.70	F	gatA-Glu tRNA Gln Amidotransferae-(CT003)
CPn0004	2370	3833	F	gatB-(Pet 112) Glu tRNA Gln Amidotransferase (B Subunit)
CPn005	4127	6892	F	pmp_1-Polymorphic Outer Membrane Protein G Family
CPn006	7293	7141	R	
CPn007	7605	10496	F	
CPn008	10975	11685	F	
CPn009	11815	13119	F	
CPn0010	13435	14325	F	
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	. F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP [leader (14) peptide: outer membrane] - (CT351)
CPn0021	34410	32707	R	Predicted OMP [leader (19) peptide] - (CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R .	yjjK/alr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	R	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	Ion-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0038	52119	53831	F	pts1-PTS PEP Phosphotransferase-(CT336)
CPn0039	54250	53963 REF	R LACEMEN	ybaB-(CT335) JT PAGE 37 (2 of 2)
		1001		/





:		t RNAs		
tRNA #	Begin	End	Туре	Codon
ı	89657	89728	Thr	CCT
2	90998	91070	Trp	CCA
	1.49323	1 # 301	Mest	·
1	199717	Elements.	Meet	CAT
5	296075	296147	Val	TAC
6	296151	296224	Asp	CTC
7	409848	409922	Pro	TGG
. 8	462141	462214	Arg	CCT
9	672236	672318	Leu	CAA
10	677264	677337	Arg	TCG
11	739403	739486	Leu	CAG
12	781610	781680	Gly	TCC
13	784822	784896	Glu	TTC
14	784922	784994	Lys	TTT
15	836119	836191	Ala	GGC
16	843926	843999	Pro	GGG
17	877400	877473	Arg	ACG
18	1085605	1085676	Gln	TTG
19	1142034	1142118	Ser	TGA
20	1175863	1175944	Leu	TAG
21	1230028	1229942	Ser	CGA
22	1137462	1137389	Val	GAC
23	1030603	1030533	Cys	GCA
24	1000022	999949	His	GTG
25	961607	961536	Gly	GCC
26	807413	807341	Arg	TCT
27	786780	786708	Thr	CCT
28	715971	715889	Leu	TAA
29	708441	708354	Ser	GCT
30	680259	680178	Leu	GAG
31	631445	631373	Phe	GAA
32	626987	626901	Ser	GGA
33	293477	293405	Thr	TGT
34	293399	293317	Tyr	GTA
35	269142	269070	Ala	TGC
36	269065	268992	Ile	GAT
37	164389	164318	Asn	GTT
38	87522	87450	Met	CAT

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ANNOTATED PAGE 123



TABLE 2

```
Gene Function (C. trachomatis ortholog in parentheses)
                                        CT001 hypothetical protein
           282
                                   R
CPn0001
                                        gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002)
                       875
           573
                                   F
CPn0002
                                        gatA-Glu tRNA Gln Amidotransferae-(CT003)
           895
                       2370
CPn0003
                                        gat8-(Petil2) GlockPNA Glo Amidotransferase (8 Subunit)-(CT904)
                       1 6 1 3
           2170
 Pad004
                                        pmp_1-Polymorphic Outer Membrane Protein G Family
                       6892
           4127
CPNUUU5
                       7141
           7293
CPn0006
                       10496
CPn0007
           7605
                       11685
CPn0008
           10975
                                                                                             SEP 9
                                                                                                       2003
                       13119
CPn0409
           11815
                       14325
CPn0010
           13435
                                                                                       TECH CENTER 1600/2900
                                        frame-shift with 0010
                       15746
CPn0010
           14379
                       16614
CPn001%
           15892
           16644
                       18212
CPn0012
                                        pmp_2-Polymorphic Outer Membrane Protein G Family
                       21106
CPn0013
           18584
                                        pmp_3-Polymorphic Outer Membrane Protein G Family
           21392
                       21922
CPn0014
                                        pmp_3-PMP_3 (frame-shift with 0014)
                       24174
CPn0015
           21835
                                        pmp_4-Polymorphic Outer Membrane Protein G Family
           24416
                       26188
CPn0016
                                        pmp_4-PMP_4 (frame-shift with 0016)
                       27170
           26094
CPn0017
                                        pmp_5-Polymorphic Outer Membrane Protein G Family
           27522
                       29003
CPn0018
                                        pmp_5-PMP_5 (frame-shift with 0018)
           29007
                       30356
CPn0019
                                        Predicted OMP [leader (14) peptide: outer membrane]-(CT351)
                       30603
           32687
CPn0020
                                        Predicted OMP (leader (19) peptide]-(CT350)
                       32707
CPn0021
           34410
                       34395
                                        maf-(CT349)
CPn0022
           34982
                                        yjjK/alr-ABC Transporter Protein ATPase-(CT348)
                       35014
CPn0023
           36603
                                        xerC-Integrase/recombinase-(CT347)
                       36661
CPn0024
           37596
                                        elaC/atsA-Sulphohydrolase/Glycosulfatase-( CT346)
           38604
                       37684
CPn0025
                                        CT345 hypothetical protein-(CT345)
CPn0026
           39625
                       38762
                                  R
                                        lon-Lon ATP-dependent Protease-(CT344)
           42234
                       39778
                                  R
CPn0027
           43325
                       42543
CPn0028
           43755
                       43390
CPn0029
                                        gcp_1-0-Sialoglycoprotein Endopeptidase_1-(CT343)
                       44529
                                  P
CPn0030
           43891
                                        rs21-S21 Ribosomal Protein-(CT342)
                       44884
CPn0031
           44711
                                        dnaJ-Heat Shock Protein J-(CT341)
CPn0032
           44923
                       46098
                                  F
                                        pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta
                       48171
                                  F
CPn0033
           46138
                                           Pusion-(CT340)
           49457
                       48210
                                  R
CPn0034
                                        CT339 hypothetical protein
CPn0035
           51029
                       49569
                                  R
                                        CT338 hypothetical protein
                       51796
           51002
                                  F
CPn0036
                                        ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0037
           51792
                       52115
                                        ptsI-PTS PEP Phosphotransferase-(CT336)
                       53831
CPn0038
           52119
                                  F
                                        ybaB-(CT335)
CPn0039
           54250
                       53963
                                  R
                                        dnaX_1-DNA Pol III Gamma and Tau_1-(CT334)
CPn0040
           55643
                       54318
                                  R
           55996
                       57342
CPn0041
CPn0042
           57403
                       58182
           58447
                       60372
                                                         BEST AVAILABLE COPY
CPn0043
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                       60778
CPn0044
                       62790
CPn0045
           61069
           62790
                       63263
CPn0046
                       63652
                                  r
CPn0047
           63455
                                        *yqfF-Bs conserved hypothetical IM protein
CPn0048
           63687
                       65801
           66296
                       65817
CPn0049
                                  R
                       66499
CPn0050
           66813
CPn0051
           66833
                       67111
                                        hemC-Porphobilinogen Deaminase-(CT299)
           68005
                       67304
CPn0052
                                        sms-Sms Protein-(CT298)
                       67986
           69344
CPn0053
                                        rnc-Ribonuclease III-(CT297)
CPn0054
           70023
                       69313
                                        CT296 hypothetical protein
                       70590
           70129
CPn0055
                                        mrsA-Phosphomannomutase-(CT295)
CPn0056
           70953
                       72746
                                        sodM-Superoxide Dismutase (Mn)-(CT294)
                       73554
           77934
CPn0057
                                        accD-AcCoA Carboxylase/Transferase Beta-(CT293)
CPn0058
           73639
                       74562
                                        dut-duty Nucleotidohydrolase-(CT292)
CPn0059
                       75050
           74616
                                        ptsN_1-PTS [IA Protein-(CT291)
CPn0060
           75055
                       75528
                                        ptsN_2-PTS IIA Protein + HTH DNA-Binding Domain-(CT290)
CPn0051
           75514
                       76208
                                        CT289 hypothetical protein
CPn0062
           76308
                       77690
                       78267
C2n0063
           78L12
                       78576
CPn0064
           74346
                                        CT188 hypothesical procein
                       4065 L
CPn0065
           78924
                       82655
C2n0056
           H0925
```